

Sequence listing

<110> Pieris Proteolab AG

<120> Soluble truncated polypeptides of the Nogo-A protein, methods for the production of such polypeptides and methods for identifying compounds having detectable affinity to a Nogo-A protein

<160> 18

<210> 1
<211> 1163
<212> PRT
<213> rat

<220>
<223> rat Nogo-A protein

<400> 1

Met Glu Asp Ile Asp Gln Ser Ser Leu Val Ser Ser Ser Thr Asp
1 5 10 15

Ser Pro Pro Arg Pro Pro Pro Ala Phe Lys Tyr Gln Phe Val Thr
20 25 30

Glu Pro Glu Asp Glu Glu Asp Glu Glu Glu Glu Asp Glu Glu
35 40 45

Glu Asp Asp Glu Asp Leu Glu Glu Leu Glu Val Leu Glu Arg Lys
50 55 60

Pro Ala Ala Gly Leu Ser Ala Ala Ala Val Pro Pro Ala Ala Ala
65 70 75

Ala Pro Leu Leu Asp Phe Ser Ser Asp Ser Val Pro Pro Ala Pro
80 .. 85 90

Arg Gly Pro Leu Pro Ala Ala Pro Pro Ala Ala Pro Glu Arg Gln
95 100 105

Pro Ser Trp Glu Arg Ser Pro Ala Ala Pro Ala Pro Ser Leu Pro
110 115 120

Pro Ala Ala Ala Val Leu Pro Ser Lys Leu Pro Glu Asp Asp Glu
125 130 135

Pro Pro Ala Arg Pro Pro Pro Pro Pro Ala Gly Ala Ser Pro
140 145 150

Leu Ala Glu Pro Ala Ala Pro Pro Ser Thr Pro Ala Ala Pro Lys
155 160 165

Arg Arg Gly Ser Gly Ser Val Asp Glu Thr Leu Phe Ala Leu Pro
170 175 180

Ala Ala Ser Glu Pro Val Ile Pro Ser Ser Ala Glu Lys Ile Met
185 190 195

Asp Leu Met Glu Gln Pro Gly Asn Thr Val Ser Ser Gly Gln Glu

200	205	210
Asp Phe Pro Ser Val Leu Leu Glu Thr Ala Ala Ser Leu Pro Ser		
215	220	225
Leu Ser Pro Leu Ser Thr Val Ser Phe Lys Glu His Gly Tyr Leu		
230	235	240
Gly Asn Leu Ser Ala Val Ser Ser Ser Glu Gly Thr Ile Glu Glu		
245	250	255
Thr Leu Asn Glu Ala Ser Lys Glu Leu Pro Glu Arg Ala Thr Asn		
260	265	270
Pro Phe Val Asn Arg Asp Leu Ala Glu Phe Ser Glu Leu Glu Tyr		
275	280	285
Ser Glu Met Gly Ser Ser Phe Lys Gly Ser Pro Lys Gly Glu Ser		
290	295	310
Ala Ile Leu Val Glu Asn Thr Lys Glu Glu Val Ile Val Arg Ser		
305	310	315
Lys Asp Lys Glu Asp Leu Val Cys Ser Ala Ala Leu His Ser Pro		
320	325	330
Gln Glu Ser Pro Val Gly Lys Glu Asp Arg Val Val Ser Pro Glu		
335	340	345
Lys Thr Met Asp Ile Phe Asn Glu Met Gln Met Ser Val Val Ala		
350	355	360
Pro Val Arg Glu Glu Tyr Ala Asp Phe Lys Pro Phe Glu Gln Ala		
365	370	375
Trp Glu Val Lys Asp Thr Tyr Glu Gly Ser Arg Asp Val Leu Ala		
380	385	390
Ala Arg Ala Asn Val Glu Ser Lys Val Asp Arg Lys Cys Leu Glu		
395	400	405
Asp Ser Leu Glu Gln Lys Ser Leu Gly Lys Asp Ser Glu Gly Arg		
410	415	420
Asn Glu Asp Ala Ser Phe Pro Ser Thr Pro Glu Pro Val Lys Asp		
425	430	435
Ser Ser Arg Ala Tyr Ile Thr Cys Ala Ser Phe Thr Ser Ala Thr		
440	445	450
Glu Ser Thr Thr Ala Asn Thr Phe Pro Leu Leu Glu Asp His Thr		
455	460	465
Ser Glu Asn Lys Thr Asp Glu Lys Lys Ile Glu Glu Arg Lys Ala		
470	475	480
Gln Ile Ile Thr Glu Lys Thr Ser Pro Lys Thr Ser Asn Pro Phe		
485	490	495
Leu Val Ala Val Gln Asp Ser Glu Ala Asp Tyr Val Thr Thr Asp		
500	505	510
Thr Leu Ser Lys Val Thr Glu Ala Ala Val Ser Asn Met Pro Glu		

515	520	525
Gly Leu Thr Pro Asp Leu Val Gln Glu Ala Cys Glu Ser Glu Leu		
530	535	540
Asn Glu Ala Thr Gly Thr Lys Ile Ala Tyr Glu Thr Lys Val Asp		
545	550	555
Leu Val Gln Thr Ser Glu Ala Ile Gln Glu Ser Leu Tyr Pro Thr		
560	565	570
Ala Gln Leu Cys Pro Ser Phe Glu Glu Ala Glu Ala Thr Pro Ser		
575	580	585
Pro Val Leu Pro Asp Ile Val Met Glu Ala Pro Leu Asn Ser Leu		
590	595	600
Leu Pro Ser Ala Gly Ala Ser Val Val Gln Pro Ser Val Ser Pro		
605	610	615
Leu Glu Ala Pro Pro Pro Val Ser Tyr Asp Ser Ile Lys Leu Glu		
620	625	630
Pro Glu Asn Pro Pro Pro Tyr Glu Glu Ala Met Asn Val Ala Leu		
635	640	645
Lys Ala Leu Gly Thr Lys Glu Gly Ile Lys Glu Pro Glu Ser Phe		
650	655	660
Asn Ala Ala Val Gln Glu Thr Glu Ala Pro Tyr Ile Ser Ile Ala		
665	670	675
Cys Asp Leu Ile Lys Glu Thr Lys Leu Ser Thr Glu Pro Ser Pro		
680	685	690
Asp Phe Ser Asn Tyr Ser Glu Ile Ala Lys Phe Glu Lys Ser Val		
695	700	705
Pro Glu His Ala Glu Leu Val Glu Asp Ser Ser Pro Glu Ser Glu		
710	715	720
Pro Val Asp Leu Phe Ser Asp Asp Ser Ile Pro Glu Val Pro Gln		
725	730	735
Thr Gln Glu Glu Ala Val Met Leu Met Lys Glu Ser Leu Thr Glu		
740	745	750
Val Ser Glu Thr Val Ala Gln His Lys Glu Glu Arg Leu Ser Ala		
755	760	765
Ser Pro Gln Glu Leu Gly Lys Pro Tyr Leu Glu Ser Phe Gln Pro		
770	775	780
Asn Leu His Ser Thr Lys Asp Ala Ala Ser Asn Asp Ile Pro Thr		
785	790	795
Leu Thr Lys Lys Glu Lys Ile Ser Leu Gln Met Glu Glu Phe Asn		
800	805	810
Thr Ala Ile Tyr Ser Asn Asp Asp Leu Leu Ser Ser Lys Glu Asp		
815	820	825
Lys Ile Lys Glu Ser Glu Thr Phe Ser Asp Ser Ser Pro Ile Glu		

830	835	840
Ile Ile Asp Glu Phe Pro Thr Phe Val Ser Ala Lys Asp Asp Ser		
845	850	855
Pro Lys Leu Ala Lys Glu Tyr Thr Asp Leu Glu Val Ser Asp Lys		
860	865	870
Ser Glu Ile Ala Asn Ile Gln Ser Gly Ala Asp Ser Leu Pro Cys		
875	880	885
Leu Glu Leu Pro Cys Asp Leu Ser Phe Lys Asn Ile Tyr Pro Lys		
890	895	900
Asp Glu Val His Val Ser Asp Glu Phe Ser Glu Asn Arg Ser Ser		
905	910	915
Val Ser Lys Ala Ser Ile Ser Pro Ser Asn Val Ser Ala Leu Glu		
920	925	930
Pro Gln Thr Glu Met Gly Ser Ile Val Lys Ser Lys Ser Leu Thr		
935	940	945
Lys Glu Ala Glu Lys Lys Leu Pro Ser Asp Thr Glu Lys Glu Asp		
950	955	960
Arg Ser Leu Ser Ala Val Leu Ser Ala Glu Leu Ser Lys Thr Ser		
965	970	975
Val Val Asp Leu Leu Tyr Trp Arg Asp Ile Lys Lys Thr Gly Val		
980	985	990
Val Phe Gly Ala Ser Leu Phe Leu Leu Leu Ser Leu Thr Val Phe		
995	1000	1005
Ser Ile Val Ser Val Thr Ala Tyr Ile Ala Leu Ala Leu Leu Ser		
1010	1015	1020
Val Thr Ile Ser Phe Arg Ile Tyr Lys Gly Val Ile Gln Ala Ile		
1030	1030	1035
Gln Lys Ser Asp Glu Gly His Pro Phe Arg Ala Tyr Leu Glu Ser		
1040	1045	1050
Glu Val Ala Ile Ser Glu Glu Leu Val Gln Lys Tyr Ser Asn Ser		
1055	1060	1065
Ala Leu Gly His Val Asn Ser Thr Ile Lys Glu Leu Arg Arg Leu		
1070	1075	1080
Phe Leu Val Asp Asp Leu Val Asp Ser Leu Lys Phe Ala Val Leu		
1085	1090	1095
Met Trp Val Phe Thr Tyr Val Gly Ala Leu Phe Asn Gly Leu Thr		
1100	1105	1110
Leu Leu Ile Leu Ala Leu Ile Ser Leu Phe Ser Ile Pro Val Ile		
1115	1120	1125
Tyr Glu Arg His Gln Val Gln Ile Asp His Tyr Leu Gly Leu Ala		
1130	1135	1140
Asn Lys Ser Val Lys Asp Ala Met Ala Lys Ile Gln Ala Lys Ile		

1145

1150

1155

Pro Gly Leu Lys Arg Lys Ala Asp
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<211> 1192
<212> PRT
<213> human

<220>
<223> human Nogo-A protein

<400> 2

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20 25 30

Pro Glu Asp Glu Glu Glu Glu Glu Glu Glu Glu Asp Glu
35 40 45

Asp Glu Asp Leu Glu Glu Leu Glu Val Leu Glu Arg Lys Pro Ala
50 55 60

Ala Gly Leu Ser Ala Ala Pro Val Pro Thr Ala Pro Ala Ala Gly
65 70 75

Ala Pro Leu Met Asp Phe Gly Asn Glu Phe Val Pro Pro Ala Pro
80 85 90

Arg Gly Pro Leu Pro Ala Ala Pro Pro Val Ala Pro Glu Arg Gln
95 100 105

Pro Ser Trp Asp Pro Ser Pro Val Ser Ser Thr Val Pro Ala Pro
110 115 120

Ser Pro Leu Ser Ala Ala Ala Val Ser Pro Ser Lys Leu Pro Glu
125 130 135

Asp Asp Glu Pro Pro Ala Arg Pro Pro Pro Pro Pro Ala Ser
140 145 150

Val Ser Pro Gln Ala Glu Pro Val Trp Thr Pro Pro Ala Pro Ala
155 160 165

Pro Ala Ala Pro Pro Ser Thr Pro Ala Ala Pro Lys Arg Arg Gly
170 185 180

Ser Ser Gly Ser Val Asp Glu Thr Leu Phe Ala Leu Pro Ala Ala
185 190 195

Ser Glu Pro Val Ile Arg Ser Ser Ala Glu Asn Met Glu Leu Lys
200 205 210

Glu Gln Pro Gly Asn Thr Ile Ser Ala Gly Gln Glu Asp Phe Pro
215 220 225

Ser Val Leu Leu Glu Thr Ala Ala Ser Leu Pro Ser Leu Ser Pro

230	235	240
Leu Ser Ala Ala Ser Phe Lys Glu His Glu Tyr Leu Glu Asn Leu		
245	250	255
Ser Thr Val Leu Pro Thr Glu Gly Thr Leu Gln Glu Asn Val Ser		
260	265	270
Glu Ala Ser Lys Glu Val Ser Glu Lys Ala Lys Thr Leu Leu Ile		
275	280	285
Asp Arg Asp Leu Thr Glu Phe Ser Glu Leu Glu Tyr Ser Glu Met		
290	295	300
Gly Ser Ser Phe Ser Val Ser Pro Lys Ala Glu Ser Ala Val Ile		
305	310	315
Val Ala Asn Pro Arg Glu Glu Ile Ile Val Lys Asn Lys Asp Glu		
320	325	330
Glu Glu Lys Leu Val Ser Asn Ans Ile Leu His Asn Gln Gln Glu		
335	340	345
Leu Pro Thr Ala Leu Thr Lys Leu Val Lys Glu Asp Glu Val Val		
350	355	360
Ser Ser Glu Lys Ala Lys Asp Ser Phe Asn Glu Lys Arg Val Ala		
365	370	385
Val Glu Ala Pro Met Arg Glu Glu Tyr Ala Asp Phe Lys Pro Phe		
380	385	390
Glu Arg Val Trp Glu Val Lys Asp Ser Lys Glu Asp Ser Asp Met		
395	400	405
Leu Ala Ala Gly Gly Lys Ile Glu Ser Asn Leu Glu Ser Lys Val		
410	415	420
Asp Lys Lys Cys Phe Ala Asp Ser Leu Glu Gln Thr Asn His Glu		
425	430	435
Lys Asn Ser Glu Ser Ser Asn Asp Asp Thr Ser Phe Pro Ser Thr		
440	445	450
Pro Glu Gly Ile Lys Asp Arg Pro Gly Ala Tyr Ile Thr Cys Ala		
455	460	465
Pro Phe Asn Pro Ala Ala Thr Glu Ser Ile Ala Thr Asn Ile Phe		
470	475	480
Pro Leu Leu Gly Asp Pro Thr Ser Glu Asn Lys Thr Asp Glu Lys		
485	490	495
Lys Ile Glu Glu Lys Lys Ala Gln Ile Val Thr Glu Lys Asn Thr		
500	505	510
Ser Thr Lys Thr Ser Asn Pro Phe Leu Val Ala Ala Gln Glu Ser		
515	520	525
Glu Thr Asp Tyr Val Thr Asp Asn Leu Thr Lys Val Thr Glu		
530	535	540
Glu Val Val Ala Asn Met Pro Glu Gly Leu Thr Pro Asp Leu Val		

545	550	555
Gln Glu Ala Cys Glu Ser Glu Leu Asn Glu Val Thr Gly Thr Lys		
560	565	570
Ile Ala Tyr Glu Thr Lys Met Asp Leu Val Gln Thr Ser Glu Val		
575	580	585
Met Gln Glu Ser Leu Tyr Pro Ala Ala Gln Leu Cys Pro Ser Phe		
590	595	600
Glu Glu Ser Glu Ala Thr Pro Ser Pro Val Leu Pro Asp Ile Val		
605	610	615
Met Glu Ala Pro Leu Asn Ser Ala Val Pro Ser Ala Gly Ala Ser		
620	625	630
Val Ile Gln Pro Ser Ser Ser Pro Leu Glu Ala Ser Ser Val Gln		
635	640	645
Tyr Glu Ser Ile Lys His Glu Pro Glu Asn Pro Pro Pro Tyr Glu		
650	655	660
Glu Ala Met Ser Val Ser Leu Lys Lys Val Ser Gly Ile Lys Glu		
665	670	675
Glu Ile Lys Glu Pro Glu Asn Ile Asn Ala Ala Leu Gln Glu Thr		
680	685	690
Glu Ala Pro Tyr Ile Ser Ile Ala Cys Asp Leu Ile Lys Glu Thr		
695	700	705
Lys Leu Ser Ala Glu Pro Ala Pro Glu Phe Ser Asp Tyr Ser Glu		
710	715	720
Met Ala Lys Val Glu Gln Pro Val Pro Asp His Ser Glu Leu Val		
725	730	735
Glu Asp Ser Ser Pro Asp Ser Glu Pro Val Asp Leu Phe Ser Asp		
740	745	750
Asp Ser Ile Pro Asp Val Pro Gln Lys Gln Asp Glu Thr Val Met		
755	760	765
Leu Val Lys Glu Ser Leu Thr Glu Thr Ser Phe Glu Ser Met Ile		
770	775	780
Glu Tyr Glu Gln Lys Glu Lys Leu Ser Ala Leu Pro Pro Glu Gly		
785	790	795
Gly Lys Pro Tyr Leu Glu Ser Phe Lys Leu Ser Leu Asp Asn Thr		
800	805	810
Lys Asp Thr Leu Leu Pro Asp Glu Val Ser Thr Leu Ser Lys Lys		
815	820	825
Glu Lys Ile Pro Ile Gln Met Glu Glu Leu Ser Thr Ala Val Tyr		
830	835	840
Ser Asn Asp Asp Leu Phe Ile Ser Lys Glu Ala Gln Ile Arg Glu		
845	850	855
Thr Glu Thr Phe Ser Asp Ser Ser Pro Ile Glu Ile Ile Asp Glu		

860	865	870
Phe Pro Thr Leu Ile Ser Ser Lys Thr Asp Ser Phe Ser Lys Leu		
875	880	885
Ala Arg Glu Tyr Thr Asp Leu Glu Val Ser His Lys Ser Glu Ile		
890	895	900
Ala Gln Ala Pro Asp Gly Ala Gly Ser Leu Pro Cys Thr Glu Leu		
905	910	915
Pro His Asp Leu Ser Leu Lys Asn Ile Gln Pro Lys Val Glu Glu		
920	925	930
Lys Ile Ser Phe Ser Asp Asp Phe Ser Lys Asn Gly Ser Ala Thr		
935	940	945
Ser Lys Val Leu Leu Leu Pro Pro Asp Val Ser Ala Leu Ala Thr		
950	955	960
Gln Ala Glu Ile Glu Ser Ile Val Lys Pro Lys Val Leu Val Lys		
965	970	975
Glu Ala Glu Lys Lys Leu Pro Ser Asp Thr Glu Lys Glu Asp Arg		
980	985	990
Ser Pro Ser Ala Ile Phe Ser Ala Glu Leu Ser Lys Thr Ser Val		
995	1000	1005
Val Asp Leu Leu Tyr Trp Arg Asp Ile Lys Lys Thr Gly Val Val		
1010	1015	1020
Phe Gly Ala Ser Leu Phe Leu Leu Ser Leu Thr Val Phe Ser		
1025	1030	1035
Ile Val Ser Val Thr Ala Tyr Ile Ala Leu Ala Leu Leu Ser Val		
1040	1045	1050
Thr Ile Ser Phe Arg Ile Tyr Lys Gly Val Ile Gln Ala Ile Gln		
1055	1060	1065
Lys Ser Asp Glu Gly His Pro Phe Arg Ala Tyr Leu Glu Ser Glu		
1070	1075	1080
Val Ala Ile Ser Glu Glu Leu Val Gln Lys Tyr Ser Asn Ser Ala		
1085	1090	1095
Leu Gly His Val Asn Cys Thr Ile Lys Glu Leu Arg Arg Leu Phe		
1100	1105	1110
Leu Val Asp Asp Leu Val Asp Ser Leu Lys Phe Ala Val Leu Met		
1115	1120	1125
Trp Val Phe Thr Tyr Val Gly Ala Leu Phe Asn Gly Leu Thr Leu		
1130	1135	1140
Leu Ile Leu Ala Leu Ile Ser Leu Phe Ser Val Pro Val Ile Tyr		
1145	1150	1155
Glu Arg His Gln Ala Gln Ile Asp His Tyr Leu Gly Leu Ala Asn		
1160	1165	1170
Lys Asn Val Lys Asp Ala Met Ala Lys Ile Gln Ala Lys Ile Pro		

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1180

1185

Gly Leu Lys Arg Lys Ala Glu
1190

<210> 3
<211> 33
<212> DNA
<213> artificial sequence

<220>
<223> Primer

<400> 3

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<210> 4
<211> 27
<212> DNA
<213> artificial sequence

<220>
<223> Primer

<400> 4

gcttttaact atgctgccca tttctgt 27

<210> 5
<211> 40
<212> DNA
<213> artificial sequence

<220>
<223> Primer

<400> 5

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<211> 63
<212> DNA
<213> artificial sequence

<220>
<223> Primer

<400> 6

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aactatgctg ccc 63

<210> 7
<211> 42
<212> DNA
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<220>
<223> Primer

<400> 7

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42

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<211> 39
<212> DNA
<213> artificial sequence

<220>
<221> misc_feature
<222> (34)
<223> k: g or t

<220>
<223> Primer

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39

<210> 9
<211> 66
<212> DNA
<213> artificial sequence

<220>
<221> misc_feature
<222> (37) ... (39)
<223> n: a, g, c or t; m: a or c

<220>
<221> misc_feature
<222> (43) ... (48)

<223> n: a, g, c or t; m: a or c

<220>
<223> Primer

<400> 9

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acacattttg acagta

50

66

<210> 10
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<212> DNA
<213> artificial sequence

<220>
<221> misc_feature
<222> (49) ... (54)
<223> n: a, g, c or t; m: a or c

<220>
<223> Primer

<400> 10

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nmnnnatttg acagtaatac gttgc 74

<210> 11
<211> 121
<212> PRT
<213> mouse

<220>
<221>
<222> (1) ... (121)
<223> variable domain of the heavy chain of antibody IN-1

<400> 11

Glu Val Lys Leu His Glu Ser Gly Pro Gly Leu Val Arg Pro Gly
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Thr Ser Val Lys Ile Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr
20 25 30

Asn Tyr Trp Leu Gly Trp Val Lys Gln Arg Pro Gly His Gly Leu
35 40 45

Glu Trp Ile Gly Asp Ile Tyr Pro Gly Gly Gly Tyr Thr Asn Tyr
50 55 60

Asn Glu Lys Phe Lys Gly Lys Ala Thr Leu Thr Ala Asp Thr Ser
65 70 75

Ser Ser Thr Ala Tyr Met Gln Leu Ser Ser Leu Thr Ser Glu Asp
80 85 90

Ser Ala Val Tyr Phe Cys Ala Arg Phe Tyr Tyr Gly Ser Ser Tyr
95 100 105

Trp Tyr Phe Asp Val Trp Gly Gln Gly Thr Thr Val Thr Val Ser
110 115 120

Ser

<210> 12
<211> 107
<212> PRT
<213> artificial sequence

<220>
<221>
<222> (1) ... (107)

<223> variable domain of the light chain of the antibody II.1.8

<400> 12

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Gly	Glu	Thr	Val	Thr	Ile	Thr	Cys	Gly	Ala	Ser	Glu	Asn	Ile	Tyr
					20				25					30

Gly	Ala	Leu	Asn	Trp	Tyr	Gln	Arg	Lys	Gln	Gly	Lys	Ser	Pro	Gln
					35				40					45

Leu	Leu	Ile	Tyr	Gly	Ala	Thr	Asn	Leu	Ala	Asp	Gly	Met	Ser	Ser
					50				55					60

Arg	Phe	Ser	Gly	Ser	Gly	Ser	Gly	Arg	Gln	Tyr	Ser	Leu	Lys	Ile
					65				70					75

Ser	Ser	Leu	His	Pro	Asp	Asp	Val	Ala	Thr	Tyr	Tyr	Cys	Gln	Asn
					80				85					90

Ile	Asn	Arg	Val	Pro	Val	Thr	Phe	Ala	Gly	Thr	Lys	Leu	Glu	
					95				100					105

Ile Lys

<210> 13

<211> 2238

<212> DNA

<213> artifical sequence ..

<220>

<221> sig_peptide

<222> (22)...(84)

<220>

<221> mat_peptide

<222> (85)...(2238)

<223> fusion protein of truncated rat Nogo-A fragment and Strep-tag II

<220>

<221> CDS

<222> (85)...(2208)

<223> mature truncated Nogo-A

<220>

<221> CDS

<222> (2209)...(2238)

<223> Strep-tag II affinity tag

<400> 13

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											Met	Lys	Lys	Thr	Ala	Ile	Ala	Ile

-21 -20 -15

gca gtg gca ctg gct ggt ttc gct acc gta gcg cag gcc tct ttt 90
 Ala Val Ala Leu Ala Gly Phe Ala Thr Val Ala Gln Ala Ser Phe
 -10 -5 -1 1

aaa gaa cat gga tac ctt ggt aac tta tca gca gtg tca tcc tca 135
 Lys Glu His Gly Tyr Leu Gly Asn Leu Ser Ala Val Ser Ser Ser
 5 10 15

gaa gga aca att gaa gaa act tta aat gaa gct tct aaa gag ttg 180
 Glu Gly Thr Ile Glu Glu Thr Leu Asn Glu Ala Ser Lys Glu Leu
 20 25 30

cca gag agg gca aca aat cca ttt gta aat aga gat tta gca gaa 225
 Pro Glu Arg Ala Thr Asn Pro Phe Val Asn Arg Asp Leu Ala Glu
 35 40 45

ttt tca gaa tta gaa tat tca gaa atg gga tca tct ttt aaa ggc 270
 Phe Ser Glu Leu Glu Tyr Ser Glu Met Gly Ser Ser Phe Lys Gly
 50 55 60

tcc cca aaa gga gag tca gcc ata tta gta gaa aac act aag gaa 315
 Ser Pro Lys Gly Glu Ser Ala Ile Leu Val Glu Asn Thr Lys Glu
 65 70 75

gaa gta att gtg agg agt aaa gac aaa gag gat tta gtt tgt agt 360
 Glu Val Ile Val Arg Ser Lys Asp Lys Glu Asp Leu Val Cys Ser
 80 85 90

gca gcc ctt cac agt cca caa gaa tca cct gtg ggt aaa gaa gac 405
 Ala Ala Leu His Ser Pro Gln Glu Ser Pro Val Gly Lys Glu Asp
 95 100 105

aga gtt gtg tct cca gaa aag aca atg gac att ttt aat gaa atg 450
 Arg Val Val Ser Pro Glu Lys Thr Met Asp Ile Phe Asn Glu Met
 110 115 120

cag atg tca gta gta gca cct gtg agg gaa gag tat gca gac ttt 495
 Gln Met Ser Val Val Ala Pro Val Arg Glu Glu Tyr Ala Asp Phe
 125 130 135

aag cca ttt gaa caa gca tgg gaa gtg aaa gat act tat gag gga 540
 Lys Pro Phe Glu Gln Ala Trp Glu Val Lys Asp Thr Tyr Glu Gly
 140 145 150

agt agg gat gtg ctg gct gct aga gct aat gtg gaa agt aaa gtg 585
 Ser Arg Asp Val Leu Ala Ala Arg Ala Asn Val Glu Ser Lys Val
 155 160 165

gac aga aaa tgc ttg gaa gat agc ctg gag caa aaa agt ctt ggg 630
 Asp Arg Lys Cys Leu Glu Asp Ser Leu Glu Gln Lys Ser Leu Gly
 170 175 180

aag gat agt gaa ggc aga aat gag gat gct tct ttc ccc agt acc 675
 Lys Asp Ser Glu Gly Arg Asn Glu Asp Ala Ser Phe Pro Ser Thr
 185 190 195

cca gaa cct gtg aag gac agc tcc aga gca tat att acc tgt gct 720
 Pro Glu Pro Val Lys Asp Ser Ser Arg Ala Tyr Ile Thr Cys Ala
 200 205 210

tcc ttt acc tca gca acc gaa agc acc aca gca aac act ttc cct 765

Ser Phe Thr Ser Ala Thr Glu Ser Thr Thr Ala Asn Thr Phe Pro
 215 220 225
 ttg tta gaa gat cat act tca gaa aat aaa aca gat gaa aaa aaa 810
 Leu Leu Glu Asp His Thr Ser Glu Asn Lys Thr Asp Glu Lys Lys
 230 235 240
 ata gaa gaa agg aag gcc caa att ata aca gag aag act agc ccc 855
 Ile Glu Glu Arg Lys Ala Gin Ile Ile Thr Glu Lys Thr Ser Pro
 245 250 255
 aaa acg tca aat cct ttc ctt gta gca gta cag gat tct gag gca 900
 Lys Thr Ser Asn Pro Phe Leu Val Ala Val Gln Asp Ser Glu Ala
 260 265 270
 gat tat gtt aca aca gat acc tta tca aag gtg act gag gca gca 945
 Asp Tyr Val Thr Asp Thr Leu Ser Lys Val Thr Glu Ala Ala
 275 280 285
 gtg tca aac atg cct gaa ggt ctg acg cca gat tta gtt cag gaa 990
 Val Ser Asn Met Pro Glu Gly Leu Thr Pro Asp Leu Val Gln Glu
 290 295 300
 gca tgt gaa agt gaa ctg aat gaa gcc aca ggt aca aag att gct 1035
 Ala Cys Glu Ser Glu Leu Asn Glu Ala Thr Gly Thr Lys Ile Ala
 305 310 315
 tat gaa aca aaa gtg gac ttg gtc caa aca tca gaa gct ata caa 1080
 Tyr Glu Thr Lys Val Asp Leu Val Gln Thr Ser Glu Ala Ile Gln
 320 325 330
 gaa tca ctt tac ccc aca gca cag ctt tgc cca tca ttt gag gaa 1125
 Glu Ser Leu Tyr Pro Thr Ala Gln Leu Cys Pro Ser Phe Glu Glu
 335 340 345
 gct gaa gca act ccg tca cca gtt ttg cct gat att gtt atg gaa 1170
 Ala Glu Ala Thr Pro Ser Pro Val Leu Pro Asp Ile Val Met Glu
 350 355 360
 gca cca tta aat tct ctc ctt cca agc gct ggt gct tct gta gtg 1215
 Ala Pro Leu Asn Ser Leu Leu Pro Ser Ala Gly Ala Ser Val Val
 365 370 375
 cag ccc agt gta tcc cca ctg gaa gca cct cct cca gtt agt tat 1260
 Gln Pro Ser Val Ser Pro Leu Glu Ala Pro Pro Pro Val Ser Tyr
 380 385 390
 gac agt ata aag ctt gag cct gaa aac ccc cca cca tat gaa gaa 1305
 Asp Ser Ile Lys Leu Glu Pro Glu Asn Pro Pro Pro Tyr Glu Glu
 395 400 405
 gcc atg aat gta gca cta aaa gct ttg gga aca aag gaa gga ata 1350
 Ala Met Asn Val Ala Leu Lys Ala Leu Gly Thr Lys Glu Gly Ile
 410 415 420
 aaa gag cct gaa agt ttt aat gca gct gtt cag gaa aca gaa gct 1395
 Lys Glu Pro Glu Ser Phe Asn Ala Ala Val Gln Glu Thr Glu Ala
 425 430 435
 cct tat ata tcc att gcg tgt gat tta att aaa gaa aca aag ctc 1440
 Pro Tyr Ile Ser Ile Ala Cys Asp Leu Ile Lys Glu Thr Lys Leu
 440 445 450

tcc act gag cca agt cca gat ttc tct aat tat tca gaa ata gca 1485
 Ser Thr Glu Pro Ser Pro Asp Phe Ser Asn Tyr Ser Glu Ile Ala
 455 460 465

aaa ttc gag aag tcg gtg ccc gaa cac gct gag cta gtg gag gat 1530
 Lys Phe Glu Lys Ser Val Pro Glu His Ala Glu Leu Val Glu Asp
 470 475 480

tcc tca cct gaa tct gaa cca gtt gac tta ttt agt gat gat tcg 1575
 Ser Ser Pro Glu Ser Glu Pro Val Asp Leu Phe Ser Asp Asp Ser
 485 490 495

att cct gaa gtc cca caa aca caa gag gag gct gtg atg ctc atg 1620
 Ile Pro Glu Val Pro Gln Thr Gln Glu Glu Ala Val Met Leu Met
 500 505 510

aag gag agt ctc act gaa gtg tct gag aca gta gcc cag cac aaa 1665
 Lys Glu Ser Leu Thr Glu Val Ser Glu Thr Val Ala Gln His Lys
 515 520 525

gag gag aga ctt agt gcc tca cct cag gag cta gga aag cca tat 1710
 Glu Glu Arg Leu Ser Ala Ser Pro Gln Glu Leu Gly Lys Pro Tyr
 530 535 540

tta gag tct ttt cag ccc aat tta cat agt aca aaa gat gct gca 1755
 Leu Glu Ser Phe Gln Pro Asn Leu His Ser Thr Lys Asp Ala Ala
 545 550 555

tct aat gac att cca aca ttg acc aaa aag gag aaa att tct ttg 1800
 Ser Asn Asp Ile Pro Thr Leu Thr Lys Lys Glu Lys Ile Ser Leu
 560 565 570

caa atg gaa gag ttt aat act gca att tat tca aat gat gac tta 1845
 Gln Met Glu Glu Phe Asn Thr Ala Ile Tyr Ser Asn Asp Asp Leu
 575 580 585

ctt tct tct aag gaa gac aaa ata aaa gaa agt gaa aca ttt tca 1890
 Leu Ser Ser Lys Glu Asp Lys Ile Lys Glu Ser Glu Thr Phe Ser
 590 595 600

gat tca tct ccg att gag ata ata gat gaa ttt ccc acg ttt gtc 1935
 Asp Ser Ser Pro Ile Glu Ile Ile Asp Glu Phe Pro Thr Phe Val
 605 610 615

agt gct aaa gat gat tct cct aaa tta gcc aag gag tac act gat 1980
 Ser Ala Lys Asp Asp Ser Pro Lys Leu Ala Lys Glu Tyr Thr Asp
 620 625 630

cta gaa gta tcc gac aaa agt gaa att gct aat atc caa agc ggg 2025
 Leu Glu Val Ser Asp Lys Ser Glu Ile Ala Asn Ile Gln Ser Gly
 635 640 645

gca gat tca ttg cct tgc tta gaa ttg ccc tgt gac ctt tct ttc 2070
 Ala Asp Ser Leu Pro Cys Leu Glu Leu Pro Cys Asp Leu Ser Phe
 650 655 660

aag aat ata tat cct aaa gat gaa gta cat gtt tca gat gaa ttc 2115
 Lys Asn Ile Tyr Pro Lys Asp Glu Val His Val Ser Asp Glu Phe
 665 670 675

tcc gaa aat agg tcc agt gta tct aag gca tcc ata tcg cct tca 2160
 Ser Glu Asn Arg Ser Ser Val Ser Lys Ala Ser Ile Ser Pro Ser
 680 685 690

aat gtc tct gct ttg gaa cct cag aca gaa atg ggc agc ata gtt 2205
 Asn Val Ser Ala Leu Glu Pro Gln Thr Glu Met Gly Ser Ile Val
 695 700 705

aaa agc gct tgg cgt cac ccg cag ttc ggt ggt taa taa gctt 2248
 Lys Ser Ala Trp Arg His Pro Gln Phe Gly Gly End
 710 715

<210> 14
 <211> 2470
 <212> DNA
 <213> artifical sequence

<220>
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 <222> (22)...(84)

<220>
 <221> mat_peptide
 <222> (85)...(2460)
 <223> fusion protein of truncated rat Nogo-A fragment and Strep-tag II

<220>
 <221> CDS
 <222> (85)...(2430)
 <223> mature truncated Nogo-A

<220>
 <221> CDS
 <222> (2431)...(2460)
 <223> Strep-tag II affinity tag

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 -21 -20 -15

gca gtg gca ctg gct ggt ttc gct acc gta gcg cag gcc gag acc 90
 Ala Val Ala Leu Ala Gly Phe Ala Thr Val Ala Gln Ala Glu Thr
 -10 . . -5 -1 1

gct ctt cct gct gca tct gag cct gtg ata ccc tcc tct gca gaa 135
 Ala Leu Pro Ala Ala Ser Glu Pro Val Ile Pro Ser Ser Ala Glu
 5 10 15

ctt ttt aaa att atg gat ttg atg gag cag cca ggt aac act gtt 225
 Leu Phe Lys Ile Met Asp Leu Met Glu Gln Pro Gly Asn Thr Val
 20 25 30

tcg tct ggt caa gag gat ttc cca tct gtc ctg ctt gaa act gct 270
 Ser Ser Gly Gln Glu Asp Phe Pro Ser Val Leu Leu Glu Thr Ala
 35 40 45

gcc tct ctt cct tct cta tct cct ctc tca act gtt tct ttt aaa 315
 Ala Ser Leu Pro Ser Leu Ser Pro Leu Ser Thr Val Ser Phe Lys

50	55	60
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gaa cat gga tac ctt ggt aac tta tca gca gtg tca tcc tca gaa 360
 Glu His Gly Tyr Leu Gly Asn Leu Ser Ala Val Ser Ser Ser Glu
 65 70 75

gga aca att gaa gaa act tta aat gaa gct tct aaa gag ttg cca 405
 Gly Thr Ile Glu Glu Thr Leu Asn Glu Ala Ser Lys Glu Leu Pro
 80 85 90

gag agg gca aca aat cca ttt gta aat aga gat tta gca gaa ttt 450
 Glu Arg Ala Thr Asn Pro Phe Val Asn Arg Asp Leu Ala Glu Phe
 95 100 105

tca gaa tta gaa tat tca gaa atg gga tca tct ttt aaa ggc tcc 495
 Ser Glu Leu Glu Tyr Ser Glu Met Gly Ser Ser Phe Lys Gly Ser
 110 115 120

cca aaa gga gag tca gcc ata tta gta gaa aac act aag gaa gaa 540
 Pro Lys Gly Glu Ser Ala Ile Leu Val Glu Asn Thr Lys Glu Glu
 125 130 135

gta att gtg agg agt aaa gac aaa gag gat tta gtt tgt agt gca 585
 Val Ile Val Arg Ser Lys Asp Lys Glu Asp Leu Val Cys Ser Ala
 140 145 150

gcc ctt cac agt cca caa gaa tca cct gtg ggt aaa gaa gac aga 630
 Ala Leu His Ser Pro Gln Glu Ser Pro Val Gly Lys Glu Asp Arg
 155 160 165

gtt gtg tct cca gaa aag aca atg gac att ttt aat gaa atg cag 675
 Val Val Ser Pro Glu Lys Thr Met Asp Ile Phe Asn Glu Met Gln
 170 175 180

atg tca gta gta gca cct gtg agg gaa gag tat gca gac ttt aag 720
 Met Ser Val Val Ala Pro Val Arg Glu Glu Tyr Ala Asp Phe Lys
 185 190 195

cca ttt gaa caa gca tgg gaa gtg aaa gat act tat gag gga agt 765
 Pro Phe Glu Gln Ala Trp Glu Val Lys Asp Thr Tyr Glu Gly Ser
 200 205 210

agg gat gtg ctg gct gct aga gct aat gtg gaa agt aaa gtg gac 810
 Arg Asp Val Leu Ala Ala Arg Ala Asn Val Glu Ser Lys Val Asp
 215 220 225

aga aaa tgc ttg gaa gat agc ctg gag caa aaa agt ctt ggg aag 855
 Arg Lys Cys Leu Glu Asp Ser Leu Glu Gln Lys Ser Leu Gly Lys
 230 235 240

gat agt gaa ggc aga aat gag gat gct tct ttc ccc agt acc cca 900
 Asp Ser Glu Gly Arg Asn Glu Asp Ala Ser Phe Pro Ser Thr Pro
 245 250 255

gaa cct gtg aag gac agc tcc aga gca tat att acc tgt gct tcc 945
 Glu Pro Val Lys Asp Ser Ser Arg Ala Tyr Ile Thr Cys Ala Ser
 260 265 270

ttt acc tca gca acc gaa agc acc aca gca aac act ttc cct ttg 990
 Phe Thr Ser Ala Thr Glu Ser Thr Thr Ala Asn Thr Phe Pro Leu
 275 280 285

tta gaa gat cat act tca gaa aat aaa aca gat gaa aaa aaa ata 1035

Leu Glu Asp His Thr Ser Glu Asn Lys Thr Asp Glu Lys Lys Ile
 290 295 300

gaa gaa agg aag gcc caa att ata aca gag aag act agc ccc aaa 1080
 Glu Glu Arg Lys Ala Gln Ile Ile Thr Glu Lys Thr Ser Pro Lys
 305 310 315

acg tca aat cct ttc ctt gta gca gta cag gat tct gag gca gat 1125
 Thr Ser Asn Pro Phe Leu Val Ala Val Gln Asp Ser Glu Ala Asp
 320 325 330

tat gtt aca aca gat acc tta tca aag gtg act gag gca gca gtg 1170
 Tyr Val Thr Thr Asp Thr Leu Ser Lys Val Thr Glu Ala Ala Val
 335 340 345

tca aac atg cct gaa ggt ctg acg cca gat tta gtt cag gaa gca 1215
 Ser Asn Met Pro Glu Gly Leu Thr Pro Asp Leu Val Gln Glu Ala
 350 355 360

tgt gaa agt gaa ctg aat gaa gcc aca ggt aca aag att gct tat 1260
 Cys Glu Ser Glu Leu Asn Glu Ala Thr Gly Thr Lys Ile Ala Tyr
 365 370 375

gaa aca aaa gtg gac ttg gtc caa aca tca gaa gct ata caa gaa 1305
 Glu Thr Lys Val Asp Leu Val Gln Thr Ser Glu Ala Ile Gln Glu
 380 385 390

tca ctt tac ccc aca gca cag ctt tgc cca tca ttt gag gaa gct 1350
 Ser Leu Tyr Pro Thr Ala Gln Leu Cys Pro Ser Phe Glu Glu Ala
 395 400 405

gaa gca act ccg tca cca gtt ttg cct gat att gtt atg gaa gca 1395
 Glu Ala Thr Pro Ser Pro Val Leu Pro Asp Ile Val Met Glu Ala
 410 415 420

cca tta aat tct ctc ctt cca agc gct ggt gct tct gta gtg cag 1440
 Pro Leu Asn Ser Leu Leu Pro Ser Ala Gly Ala Ser Val Val Gln
 425 430 435

ccc agt gta tcc cca ctg gaa gca cct cct cca gtt agt tat gac 1485
 Pro Ser Val Ser Pro Leu Glu Ala Pro Pro Pro Val Ser Tyr Asp
 440 445 450

agt ata aag ctt gag cct gaa aac ccc cca cca tat gaa gaa gcc 1530
 Ser Ile Lys Leu Glu Pro Glu Asn Pro Pro Pro Tyr Glu Glu Ala
 455 460 465

atg aat gta gca cta aaa gct ttg gga aca aag gaa gga ata aaa 1575
 Met Asn Val Ala Leu Lys Ala Leu Gly Thr Lys Glu Gly Ile Lys
 470 475 480

gag cct gaa agt ttt aat gca gct gtt cag gaa aca gaa gct cct 1620
 Glu Pro Glu Ser Phe Asn Ala Ala Val Gln Glu Thr Glu Ala Pro
 485 490 495

tat ata tcc att gcg tgt gat tta att aaa gaa aca aag ctc tcc 1665
 Tyr Ile Ser Ile Ala Cys Asp Leu Ile Lys Glu Thr Lys Leu Ser
 500 505 510

act gag cca agt cca gat ttc tct aat tat tca gaa ata gca aaa 1710
 Thr Glu Pro Ser Pro Asp Phe Ser Asn Tyr Ser Glu Ile Ala Lys
 515 520 525

ttc gag aag tcg gtg ccc gaa cac gct gag cta gtg gag gat tcc 1755
 Phe Glu Lys Ser Val Pro Glu His Ala Glu Leu Val Glu Asp Ser
 530 535 540

 tca cct gaa tct gaa cca gtt gac tta ttt agt gat gat tcg att 1800
 Ser Pro Glu Ser Glu Pro Val Asp Leu Phe Ser Asp Asp Ser Ile
 545 550 555

 cct gaa gtc cca caa aca caa gag gag gct gtg atg ctc atg aag 1845
 Pro Glu Val Pro Gln Thr Gln Glu Glu Ala Val Met Leu Met Lys
 560 565 570

 gag agt ctc act gaa gtg tct gag aca gta gcc cag cac aaa gag 1890
 Glu Ser Leu Thr Glu Val Ser Glu Thr Val Ala Gln His Lys Glu
 575 580 585

 gag aga ctt agt gcc tca cct cag gag cta gga aag cca tat tta 1935
 Glu Arg Leu Ser Ala Ser Pro Gln Glu Leu Gly Lys Pro Tyr Leu
 590 595 600

 gag tct ttt cag ccc aat tta cat agt aca aaa gat gct gca tct 1980
 Glu Ser Phe Gln Pro Asn Leu His Ser Thr Lys Asp Ala Ala Ser
 605 610 615

 aat gac att cca aca ttg acc aaa aag gag aaa att tct ttg caa 2025
 Asn Asp Ile Pro Thr Leu Thr Lys Lys Glu Lys Ile Ser Leu Gln
 620 625 630

 atg gaa gag ttt aat act gca att tat tca aat gat gac tta ctt 2070
 Met Glu Glu Phe Asn Thr Ala Ile Tyr Ser Asn Asp Asp Leu Leu
 635 640 645

 tct tct aag gaa gac aaa ata aaa gaa agt gaa aca ttt tca gat 2115
 Ser Ser Lys Glu Asp Lys Ile Lys Glu Ser Glu Thr Phe Ser Asp
 650 655 660

 tca tct ccg att gag ata ata gat gaa ttt ccc acg ttt gtc agt 2160
 Ser Ser Pro Ile Glu Ile Ile Asp Glu Phe Pro Thr Phe Val Ser
 665 670 675

 gct aaa gat gat tct cct aaa tta gcc aag gag tac act gat cta 2205
 Ala Lys Asp Asp Ser Pro Lys Leu Ala Lys Glu Tyr Thr Asp Leu
 680 685 690

 gaa gta tcc gac aaa agt gaa att gct aat atc caa agc ggg gca 2250
 Glu Val Ser Asp Lys Ser Glu Ile Ala Asn Ile Gln Ser Gly Ala
 695 700 705

 gat tca ttg cct tgc tta gaa ttg ccc tgt gac ctt tct ttc aag 2295
 Asp Ser Leu Pro Cys Leu Glu Leu Pro Cys Asp Leu Ser Phe Lys
 710 715 720

 aat ata tat cct aaa gat gaa gta cat gtt tca gat gaa ttc tcc 2340
 Asn Ile Tyr Pro Lys Asp Glu Val His Val Ser Asp Glu Phe Ser
 725 730 735

 gaa aat agg tcc agt gta tct aag gca tcc ata tcg cct tca aat 2385
 Glu Asn Arg Ser Ser Val Ser Lys Ala Ser Ile Ser Pro Ser Asn
 740 745 750

 gtc tct gct ttg gaa cct cag aca gaa atg ggc agc ata gtt aaa 2430
 Val Ser Ala Leu Glu Pro Gln Thr Glu Met Gly Ser Ile Val Lys
 755 760 765

agc gct tgg cgt cac ccg cag ttc ggt ggt taa taa gctt 2470
 Ser Ala Trp Arg His Pro Gln Phe Gly Gly End
 770 775

<210> 15
 <211> 2281
 <212> DNA
 <213> artifical sequence

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 <221> sig_peptide
 <222> (22)...(84)

<220>
 <221> mat_peptide
 <222> (85)...(2271)
 <223> fusion protein of Strep-tag II, truncated rat Nogo-A
 fragment and hexahistidine tag

<220>
 <221> CDS
 <222> (85)...(120)
 <223> Strep-tag II affinity tag

<220>
 <221> CDS
 <222> (121)...(2250)
 <223> mature truncated Nogo-A

<220>
 <221> CDS
 <222> (2251)...(2271)
 <223> hexahistidine tag affinity tag

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 -21 -20 -15

gca gtg gca ctg gct ggt ttc gct acc gta gcg cag gcc gct agc 90
 Ala Val Ala Leu Ala Gly Phe Ala Thr Val Ala Gln Ala Ala Ser
 -10 -5 -1

tgg agc cac ccg cag ttc gaa aaa ggc gcc tct ttt aaa gaa cat 135
 Trp Ser His Pro Gln Phe Glu Lys Gly Ala Ser Phe Lys Glu His
 5 10 15

gga tac ctt ggt aac tta tca gca gtg tca tcc tca gaa gga aca 180
 Gly Tyr Leu Gly Asn Leu Ser Ala Val Ser Ser Ser Glu Gly Thr
 20 25 30

att gaa gaa act tta aat gaa gct tct aaa gag ttg cca gag agg 225
 Ile Glu Glu Thr Leu Asn Glu Ala Ser Lys Glu Leu Pro Glu Arg
 35 40 45

gca aca aat cca ttt gta aat aga gat tta gca gaa ttt tca gaa 270

Ala Thr Asn Pro Phe Val Asn Arg Asp Leu Ala Glu Phe Ser Glu
 50 55 60
 tta gaa tat tca gaa atg gga tca tct ttt aaa ggc tcc cca aaa 315
 Leu Glu Tyr Ser Glu Met Gly Ser Ser Phe Lys Gly Ser Pro Lys
 65 70 75
 gga gag tca gcc ata tta gta gaa aac act aag gaa gaa gta att 360
 Gly Glu Ser Ala Ile Leu Val Glu Asn Thr Lys Glu Glu Val Ile
 80 85 90
 gtg agg agt aaa gac aaa gag gat tta gtt tgt agt gca gcc ctt 405
 Val Arg Ser Lys Asp Lys Glu Asp Leu Val Cys Ser Ala Ala Leu
 95 100 105
 cac agt cca caa gaa tca cct gtg ggt aaa gaa gac aga gtt gtg 450
 His Ser Pro Gln Glu Ser Pro Val Gly Lys Glu Asp Arg Val Val
 110 115 120
 tct cca gaa aag aca atg gac att ttt aat gaa atg cag atg tca 495
 Ser Pro Glu Lys Thr Met Asp Ile Phe Asn Glu Met Gln Met Ser
 125 130 135
 gta gta gca cct gtg agg gaa gag tat gca gac ttt aag cca ttt 540
 Val Val Ala Pro Val Arg Glu Glu Tyr Ala Asp Phe Lys Pro Phe
 140 145 150
 gaa caa gca tgg gaa gtg aaa gat act tat gag gga agt agg gat 585
 Glu Gln Ala Trp Glu Val Lys Asp Thr Tyr Glu Gly Ser Arg Asp
 155 160 165
 gtg ctg gct aga gct aat gtg gaa agt aaa gtg gac aga aaa 630
 Val Leu Ala Ala Arg Ala Asn Val Glu Ser Lys Val Asp Arg Lys
 170 175 180
 tgc ttg gaa gat agc ctg gag caa aaa agt ctt ggg aag gat agt 675
 Cys Leu Glu Asp Ser Leu Glu Gln Lys Ser Leu Gly Lys Asp Ser
 185 190 195
 gaa ggc aga aat gag gat gct tct ttc ccc agt acc cca gaa cct 720
 Glu Gly Arg Asn Glu Asp Ala Ser Phe Pro Ser Thr Pro Glu Pro
 200 205 210
 gtg aag gac agc tcc aga gca tat att acc tgt gct tcc ttt acc 765
 Val Lys Asp Ser Ser Arg Ala Tyr Ile Thr Cys Ala Ser Phe Thr
 215 220 225
 tca gca acc gaa agc acc aca gca aac act ttc cct ttg tta gaa 810
 Ser Ala Thr Glu Ser Thr Ala Asn Thr Phe Pro Leu Leu Glu
 230 235 240
 gat cat act tca gaa aat aaa aca gat gaa aaa aaa ata gaa gaa 855
 Asp His Thr Ser Glu Asn Lys Thr Asp Glu Lys Lys Ile Glu Glu
 245 250 255
 agg aag gcc caa att ata aca gag aag act agc ccc aaa acg tca 900
 Arg Lys Ala Gln Ile Ile Thr Glu Lys Thr Ser Pro Lys Thr Ser
 260 265 270
 aat cct ttc ctt gta gca gta cag gat tct gag gca gat tat gtt 945
 Asn Pro Phe Leu Val Ala Val Gln Asp Ser Glu Ala Asp Tyr Val
 275 280 285

aca aca gat acc tta tca aag gtg act gag gca gca gtg tca aac 990
 Thr Thr Asp Thr Leu Ser Lys Val Thr Glu Ala Ala Val Ser Asn
 290 295 300

atg cct gaa ggt ctg acg cca gat tta gtt cag gaa gca tgt gaa 1035
 Met Pro Glu Gly Leu Thr Pro Asp Leu Val Gln Glu Ala Cys Glu
 305 310 315

agt gaa ctg aat gaa gcc aca ggt aca aag att gct tat gaa aca 1080
 Ser Glu Leu Asn Glu Ala Thr Gly Thr Lys Ile Ala Tyr Glu Thr
 320 325 330

aaa gtg gac ttg gtc caa aca tca gaa gct ata caa gaa tca ctt 1125
 Lys Val Asp Leu Val Gln Thr Ser Glu Ala Ile Gln Glu Ser Leu
 335 340 345

tac ccc aca gca cag ctt tgc cca tca ttt gag gaa gct gaa gca 1170
 Tyr Pro Thr Ala Gln Leu Cys Pro Ser Phe Glu Glu Ala Glu Ala
 350 355 360

act ccg tca cca gtt ttg cct gat att gtt atg gaa gca cca tta 1215
 Thr Pro Ser Pro Val Leu Pro Asp Ile Val Met Glu Ala Pro Leu
 365 370 375

aat tct ctc ctt cca agc gct ggt gct tct gta gtg cag ccc agt 1260
 Asn Ser Leu Leu Pro Ser Ala Gly Ala Ser Val Val Gln Pro Ser
 380 385 390

gta tcc cca ctg gaa gca cct cct cca gtt agt tat gac agt ata 1305
 Val Ser Pro Leu Glu Ala Pro Pro Pro Val Ser Tyr Asp Ser Ile
 395 400 405

aag ctt gag cct gaa aac ccc cca tat gaa gaa gcc atg aat 1350
 Lys Leu Glu Pro Glu Asn Pro Pro Pro Tyr Glu Glu Ala Met Asn
 410 415 420

gta gca cta aaa gct ttg gga aca aag gaa gga ata aaa gag cct 1395
 Val Ala Leu Lys Ala Leu Gly Thr Lys Glu Gly Ile Lys Glu Pro
 425 430 435

gaa agt ttt aat gca gct gtt cag gaa aca gaa gct cct tat ata 1440
 Glu Ser Phe Asn Ala Ala Val Gln Glu Thr Glu Ala Pro Tyr Ile
 440 445 450

tcc att gcg tgt gat tta att aaa gaa aca aag ctc tcc act gag 1485
 Ser Ile Ala Cys Asp Leu Ile Lys Glu Thr Lys Leu Ser Thr Glu
 455 460 465

cca agt cca gat ttc tct aat tat tca gaa ata gca aaa ttc gag 1530
 Pro Ser Pro Asp Phe Ser Asn Tyr Ser Glu Ile Ala Lys Phe Glu
 470 475 480

aag tcg gtg ccc gaa cac gct gag cta gtg gag gat tcc tca cct 1575
 Lys Ser Val Pro Glu His Ala Glu Leu Val Glu Asp Ser Ser Pro
 485 490 495

gaa tct gaa cca gtt gac tta ttt agt gat gat tcg att cct gaa 1620
 Glu Ser Glu Pro Val Asp Leu Phe Ser Asp Asp Ser Ile Pro Glu
 500 505 510

gtc cca caa aca caa gag gag gct gtg atg ctc atg aag gag agt 1665
 Val Pro Gln Thr Gln Glu Glu Ala Val Met Leu Met Lys Glu Ser
 515 520 525

ctc act gaa gtg tct gag aca gta gcc cag cac aaa gag gag aga 1710
 Leu Thr Glu Val Ser Glu Thr Val Ala Gln His Lys Glu Glu Arg
 530 535 540

ctt agt gcc tca cct cag gag cta gga aag cca tat tta gag tct 1755
 Leu Ser Ala Ser Pro Gln Glu Leu Gly Lys Pro Tyr Leu Glu Ser
 545 550 555

ttt cag ccc aat tta cat agt aca aaa gat gct gca tct aat gac 1800
 Phe Gln Pro Asn Leu His Ser Thr Lys Asp Ala Ala Ser Asn Asp
 560 565 570

att cca aca ttg acc aaa aag gag aaa att tct ttg caa atg gaa 1845
 Ile Pro Thr Leu Thr Lys Lys Glu Lys Ile Ser Leu Gln Met Glu
 575 580 585

gag ttt aat act gca att tat tca aat gat gac tta ctt tct tct 1890
 Glu Phe Asn Thr Ala Ile Tyr Ser Asn Asp Asp Leu Leu Ser Ser
 590 595 600

aag gaa gac aaa ata aaa gaa agt gaa aca ttt tca gat tca tct 1935
 Lys Glu Asp Lys Ile Lys Glu Ser Glu Thr Phe Ser Asp Ser Ser
 605 610 615

ccg att gag ata ata gat gaa ttt ccc acg ttt gtc agt gct aaa 1980
 Pro Ile Glu Ile Ile Asp Glu Phe Pro Thr Phe Val Ser Ala Lys
 620 625 630

gat gat tct cct aaa tta gcc aag gag tac act gat cta gaa gta 2025
 Asp Asp Ser Pro Lys Leu Ala Lys Glu Tyr Thr Asp Leu Glu Val
 635 640 645

tcc gac aaa agt gaa att gct aat atc caa agc ggg gca gat tca 2070
 Ser Asp Lys Ser Glu Ile Ala Asn Ile Gln Ser Gly Ala Asp Ser
 650 655 660

ttg cct tgc tta gaa ttg ccc tgt gac ctt tct ttc aag aat ata 2115
 Leu Pro Cys Leu Glu Leu Pro Cys Asp Leu Ser Phe Lys Asn Ile
 665 670 675

tat cct aaa gat gaa gta cat gtt tca gat gaa ttc tcc gaa aat 2160
 Tyr Pro Lys Asp Glu Val His Val Ser Asp Glu Phe Ser Glu Asn
 680 685 690

agg tcc agt gta tct aag gca tcc ata tcg cct tca aat gtc tct 2205
 Arg Ser Ser Val Ser Lys Ala Ser Ile Ser Pro Ser Asn Val Ser
 695 700 705

gct ttg gaa cct cag aca gaa atg ggc agc ata gtt aaa agc gct 2250
 Ala Leu Glu Pro Gln Thr Glu Met Gly Ser Ile Val Lys Ser Ala
 710 715 720

cac cat cac cat cac cat taa taa gctt
 His His His His His His End 2281
 725

<210> 16
 <211> 777
 <212> PRT

<213> artificial sequence

<220>

<221> SIGNAL

<222> (-21) ... (-1)

<220>

<221> CHAIN

<222> (1) ... (777)

<223> fusion protein of truncated rat Nogo-A fragment and Strep-tag II

<220>

<221>

<222> (1) ... (767)

<223> mature truncated Nogo-A

<220>

<221>

<222> (767) ... (777)

<223> Strep-tag II affinity tag

<400> 16

Met Lys Lys Thr Ala Ile Ala Ile
-21 -20 -15

Ala Val Ala Leu Ala Gly Phe Ala Thr Val Ala Gln Ala Glu Thr
-10 -5 -1 1

Ala Leu Pro Ala Ala Ser Glu Pro Val Ile Pro Ser Ser Ala Glu
5 10 15

Leu Phe Lys Ile Met Asp Leu Met Glu Gln Pro Gly Asn Thr Val
20 25 30

Ser Ser Gly Gln Glu Asp Phe Pro Ser Val Leu Leu Glu Thr Ala
35 40 45

Ala Ser Leu Pro Ser Leu Ser Pro Leu Ser Thr Val Ser Phe Lys
50 55 60

Glu His Gly Tyr Leu Gly Asn Leu Ser Ala Val Ser Ser Ser Glu
65 70 75

Gly Thr Ile Glu Glu Thr Leu Asn Glu Ala Ser Lys Glu Leu Pro
80 85 90

Glu Arg Ala Thr Asn Pro Phe Val Asn Arg Asp Leu Ala Glu Phe
95 100 105

Ser Glu Leu Glu Tyr Ser Glu Met Gly Ser Ser Phe Lys Gly Ser
110 115 120

Pro Lys Gly Glu Ser Ala Ile Leu Val Glu Asn Thr Lys Glu Glu
125 130 135

Val Ile Val Arg Ser Lys Asp Lys Glu Asp Leu Val Cys Ser Ala
140 145 150

Ala Leu His Ser Pro Gln Glu Ser Pro Val Gly Lys Glu Asp Arg
155 160 165

Val Val Ser Pro Glu Lys Thr Met Asp Ile Phe Asn Glu Met Gln
170 175 180

Met Ser Val Val Ala Pro Val Arg Glu Glu Tyr Ala Asp Phe Lys
185 190 195

Pro Phe Glu Gln Ala Trp Glu Val Lys Asp Thr Tyr Glu Gly Ser
200 205 210

Arg Asp Val Leu Ala Ala Arg Ala Asn Val Glu Ser Lys Val Asp
215 220 225

Arg Lys Cys Leu Glu Asp Ser Leu Glu Gln Lys Ser Leu Gly Lys
230 235 240

Asp Ser Glu Gly Arg Asn Glu Asp Ala Ser Phe Pro Ser Thr Pro
245 250 255

Glu Pro Val Lys Asp Ser Ser Arg Ala Tyr Ile Thr Cys Ala Ser
260 265 270

Phe Thr Ser Ala Thr Glu Ser Thr Thr Ala Asn Thr Phe Pro Leu
275 280 285

Leu Glu Asp His Thr Ser Glu Asn Lys Thr Asp Glu Lys Lys Ile
290 295 300

Glu Glu Arg Lys Ala Gln Ile Ile Thr Glu Lys Thr Ser Pro Lys
305 310 315

Thr Ser Asn Pro Phe Leu Val Ala Val Gln Asp Ser Glu Ala Asp
320 325 330

Tyr Val Thr Thr Asp Thr Leu Ser Lys Val Thr Glu Ala Ala Val
335 340 345

Ser Asn Met Pro Glu Gly Leu Thr Pro Asp Leu Val Gln Glu Ala
350 355 360

Cys Glu Ser Glu Leu Asn Glu Ala Thr Gly Thr Lys Ile Ala Tyr
365 370 375

Glu Thr Lys Val Asp Leu Val Gln Thr Ser Glu Ala Ile Gln Glu
380 385 390

Ser Leu Tyr Pro Thr Ala Gln Leu Cys Pro Ser Phe Glu Glu Ala
395 400 405

Glu Ala Thr Pro Ser Pro Val Leu Pro Asp Ile Val Met Glu Ala
410 415 420

Pro Leu Asn Ser Leu Leu Pro Ser Ala Gly Ala Ser Val Val Gln
425 430 435

Pro Ser Val Ser Pro Leu Glu Ala Pro Pro Pro Val Ser Tyr Asp
440 445 450

Ser Ile Lys Leu Glu Pro Glu Asn Pro Pro Pro Tyr Glu Glu Ala
455 460 465

Met Asn Val Ala Leu Lys Ala Leu Gly Thr Lys Glu Gly Ile Lys
470 475 480

Glu Pro Glu Ser Phe Asn Ala Ala Val Gln Glu Thr Glu Ala Pro
485 490 495

Tyr Ile Ser Ile Ala Cys Asp Leu Ile Lys Glu Thr Lys Leu Ser
500 505 510

Thr Glu Pro Ser Pro Asp Phe Ser Asn Tyr Ser Glu Ile Ala Lys
515 520 525

Phe Glu Lys Ser Val Pro Glu His Ala Glu Leu Val Glu Asp Ser
530 535 540

Ser Pro Glu Ser Glu Pro Val Asp Leu Phe Ser Asp Asp Ser Ile
545 550 555

Pro Glu Val Pro Gln Thr Gln Glu Glu Ala Val Met Leu Met Lys
560 565 570

Glu Ser Leu Thr Glu Val Ser Glu Thr Val Ala Gln His Lys Glu
575 580 585

Glu Arg Leu Ser Ala Ser Pro Gln Glu Leu Gly Lys Pro Tyr Leu
590 595 600

Glu Ser Phe Gln Pro Asn Leu His Ser Thr Lys Asp Ala Ala Ser
605 610 615

Asn Asp Ile Pro Thr Leu Thr Lys Lys Glu Lys Ile Ser Leu Gln
620 625 630

Met Glu Glu Phe Asn Thr Ala Ile Tyr Ser Asn Asp Asp Leu Leu
635 640 645

Ser Ser Lys Glu Asp Lys Ile Lys Glu Ser Glu Thr Phe Ser Asp
650 655 660

Ser Ser Pro Ile Glu Ile Ile Asp Glu Phe Pro Thr Phe Val Ser
665 670 675

Ala Lys Asp Asp Ser Pro Lys Leu Ala Lys Glu Tyr Thr Asp Leu
680 685 690

Glu Val Ser Asp Lys Ser Glu Ile Ala Asn Ile Gln Ser Gly Ala
695 700 705

Asp Ser Leu Pro Cys Leu Glu Leu Pro Cys Asp Leu Ser Phe Lys
710 715 720

Asn Ile Tyr Pro Lys Asp Glu Val His Val Ser Asp Glu Phe Ser
725 730 735

Glu Asn Arg Ser Ser Val Ser Lys Ala Ser Ile Ser Pro Ser Asn
740 745 750

Val Ser Ala Leu Glu Pro Gln Thr Glu Met Gly Ser Ile Val Lys
755 760 765

Ser Ala Trp Arg His Pro Gln Phe Gly Gly
770 775

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<223> fusion protein of truncated rat Nogo-A fragment and Strep-tag II

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<222> (709)...(718)
<223> Strep-tag affinity tag

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Met Lys Lys Thr Ala Ile Ala Ile
-21 -20 -15

Ala Val Ala Leu Ala Gly Phe Ala Thr Val Ala Gln Ala Ser Phe
-10 -5 -1 1

Lys Glu His Gly Tyr Leu Gly Asn Leu Ser Ala Val Ser Ser Ser
5 10 15

Glu Gly Thr Ile Glu Glu Thr Leu Asn Glu Ala Ser Lys Glu Leu
20 25 30

Pro Glu Arg Ala Thr Asn Pro Phe Val Asn Arg Asp Leu Ala Glu
35 40 45

Phe Ser Glu Leu Glu Tyr Ser Glu Met Gly Ser Ser Phe Lys Gly
50 55 60

Ser Pro Lys Gly Glu Ser Ala Ile Leu Val Glu Asn Thr Lys Glu
65 70 75

Glu Val Ile Val Arg Ser Lys Asp Lys Glu Asp Leu Val Cys Ser
80 85 90

Ala Ala Leu His Ser Pro Gln Glu Ser Pro Val Gly Lys Glu Asp
95 100 105

Arg Val Val Ser Pro Glu Lys Thr Met Asp Ile Phe Asn Glu Met
110 115 120

Gln Met Ser Val Val Ala Pro Val Arg Glu Glu Tyr Ala Asp Phe
125 130 135

Lys Pro Phe Glu Gln Ala Trp Glu Val Lys Asp Thr Tyr Glu Gly
140 145 150

Ser Arg Asp Val Leu Ala Ala Arg Ala Asn Val Glu Ser Lys Val
155 160 165

Asp Arg Lys Cys Leu Glu Asp Ser Leu Glu Gln Lys Ser Leu Gly
170 175 180

Lys Asp Ser Glu Gly Arg Asn Glu Asp Ala Ser Phe Pro Ser Thr
185 190 195

Pro Glu Pro Val Lys Asp Ser Ser Arg Ala Tyr Ile Thr Cys Ala
200 205 210

Ser Phe Thr Ser Ala Thr Glu Ser Thr Thr Ala Asn Thr Phe Pro
215 220 225

Leu Leu Glu Asp His Thr Ser Glu Asn Lys Thr Asp Glu Lys Lys
230 235 240

Ile Glu Glu Arg Lys Ala Gln Ile Ile Thr Glu Lys Thr Ser Pro
245 250 ~ 255

Lys Thr Ser Asn Pro Phe Leu Val Ala Val Gln Asp Ser Glu Ala
260 265 270

Asp Tyr Val Thr Thr Asp Thr Leu Ser Lys Val Thr Glu Ala Ala
275 280 285

Val Ser Asn Met Pro Glu Gly Leu Thr Pro Asp Leu Val Gln Glu
290 295 300

Ala Cys Glu Ser Glu Leu Asn Glu Ala Thr Gly Thr Lys Ile Ala
305 310 315

Tyr Glu Thr Lys Val Asp Leu Val Gln Thr Ser Glu Ala Ile Gln
320 325 330

Glu Ser Leu Tyr Pro Thr Ala Gln Leu Cys Pro Ser Phe Glu Glu
335 340 345

Ala Glu Ala Thr Pro Ser Pro Val Leu Pro Asp Ile Val Met Glu
350 355 360

Ala Pro Leu Asn Ser Leu Leu Pro Ser Ala Gly Ala Ser Val Val
365 370 375

Gln Pro Ser Val Ser Pro Leu Glu Ala Pro Pro Pro Val Ser Tyr
380 385 390

Asp Ser Ile Lys Leu Glu Pro Glu Asn Pro Pro Pro Tyr Glu Glu
395 400 405

Ala Met Asn Val Ala Leu Lys Ala Leu Gly Thr Lys Glu Gly Ile
410 415 420

Lys Glu Pro Glu Ser Phe Asn Ala Ala Val Gln Glu Thr Glu Ala
425 430 435

Pro Tyr Ile Ser Ile Ala Cys Asp Leu Ile Lys Glu Thr Lys Leu
440 445 450

Ser Thr Glu Pro Ser Pro Asp Phe Ser Asn Tyr Ser Glu Ile Ala
455 460 465

Lys Phe Glu Lys Ser Val Pro Glu His Ala Glu Leu Val Glu Asp
470 475 480

Ser Ser Pro Glu Ser Glu Pro Val Asp Leu Phe Ser Asp Asp Ser
485 490 495

Ile Pro Glu Val Pro Gln Thr Gln Glu Glu Ala Val Met Leu Met
500 505 510

Lys Glu Ser Leu Thr Glu Val Ser Glu Thr Val Ala Gln His Lys
515 520 525

Glu Glu Arg Leu Ser Ala Ser Pro Gln Glu Leu Gly Lys Pro Tyr
530 535 540

Leu Glu Ser Phe Gln Pro Asn Leu His Ser Thr Lys Asp Ala Ala
545 550 555

Ser Asn Asp Ile Pro Thr Leu Thr Lys Lys Glu Lys Ile Ser Leu
560 565 570

Gln Met Glu Glu Phe Asn Thr Ala Ile Tyr Ser Asn Asp Asp Leu
575 580 585

Leu Ser Ser Lys Glu Asp Lys Ile Lys Glu Ser Glu Thr Phe Ser
590 595 600

Asp Ser Ser Pro Ile Glu Ile Ile Asp Glu Phe Pro Thr Phe Val
605 610 615

Ser Ala Lys Asp Asp Ser Pro Lys Leu Ala Lys Glu Tyr Thr Asp
620 625 630

Leu Glu Val Ser Asp Lys Ser Glu Ile Ala Asn Ile Gln Ser Gly
635 640 645

Ala Asp Ser Leu Pro Cys Leu Glu Leu Pro Cys Asp Leu Ser Phe
650 655 660

Lys Asn Ile Tyr Pro Lys Asp Glu Val His Val Ser Asp Glu Phe
665 670 675

Ser Glu Asn Arg Ser Ser Val Ser Lys Ala Ser Ile Ser Pro Ser
680 685 690

Asn Val Ser Ala Leu Glu Pro Gln Thr Glu Met Gly Ser Ile Val
695 700 705

Lys Ser Ala Trp Arg His Pro Gln Phe Gly Gly
710 715